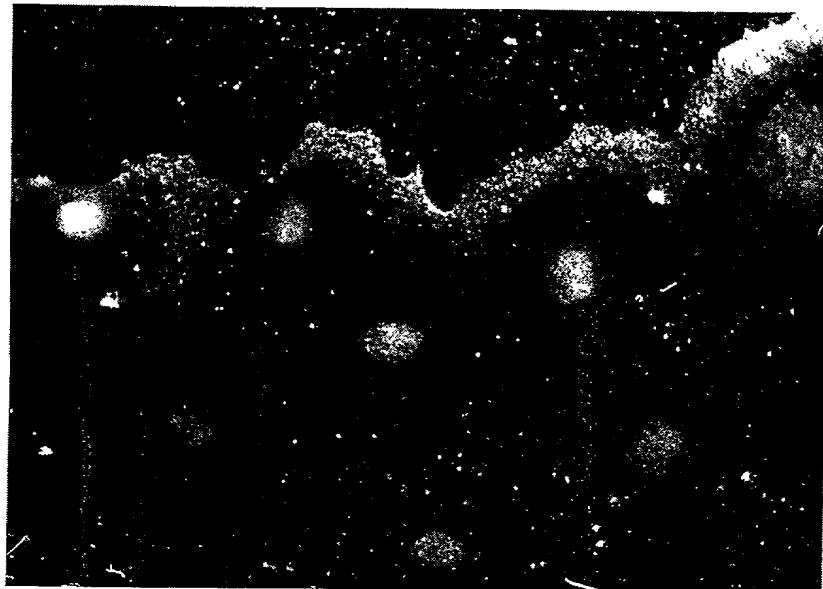
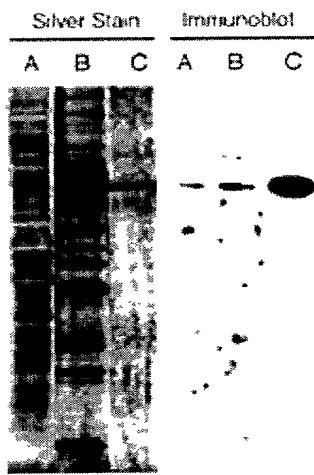


**Figure 1**



Bcap73 localizes to the forefront of endothelial cells migrating in response to injury.

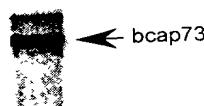
**Figure 2**



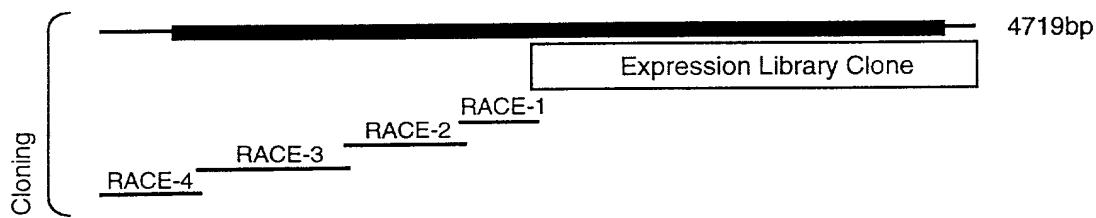
Bcap73 purification by ion-exchange chromatography.

**Figure 3**

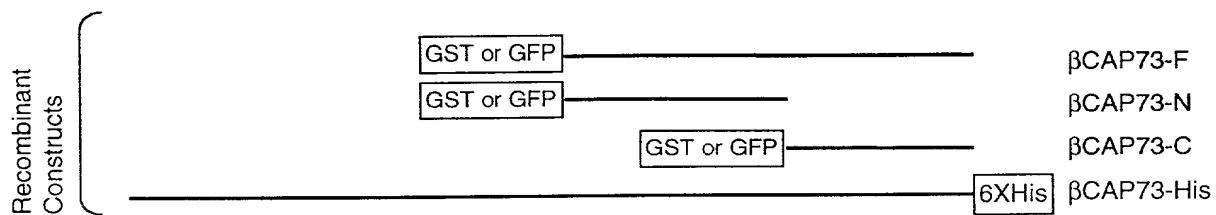
**A**



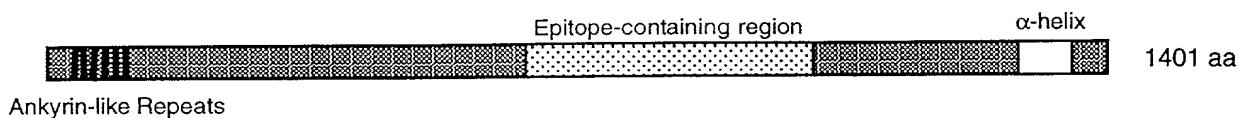
**B**



**C**



**D**



**Figure 4-1**

cagtgtttag gccccaggat gtagagtgtt caagctt tccaggag tccccaaaa 60  
 gggaaaggcag agaaagacat ctctaaata acaaataatggg gtagttacag tacctgactt 120  
 ggggctgctc ttaatcaagt gctgcccgtc caaggaagat aattttcaag cgttatgaag 180  
 gcggagaagg attccgaaga cgaagaaaat atcccttagag atccaagcta agttagtgc 240  
 agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtc ctagtttaga 300  
 gtctctctga gggctggctt tgtgagccac agtgatttgt aacttaatgc gaactaattt 360  
 gctgttagca acaagaaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412  
 Met Met Ser Cys Trp Phe Ser  
 1 5

tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460  
 Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp  
 10 15 20

cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508  
 Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser  
 25 30 35

atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556  
 Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly  
 40 45 50 55

aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604  
 Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu  
 60 65 70

aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652  
 Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Thr Ser Asp Thr Ala  
 75 80 85

gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt 700  
 Gly Arg Asn Ala Leu His Ala Ala Lys Tyr Gly His Ala Leu Cys  
 90 95 100

cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748  
 Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu  
 105 110 115

cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct 796  
 Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser  
 120 125 130 135

agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844  
 Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp  
 140 145 150

**Figure 4-2**

gta gat ggg cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca Val Asp Gly Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro 155 160 165	892
aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg 170 175 180	940
gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys 185 190 195	988
aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu 200 205 210 215	1036
ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp 220 225 230	1084
aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn 235 240 245	1132
aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn 250 255 260	1180
ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu 265 270 275	1228
cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu 280 285 290 295	1276
aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val 300 305 310	1324
aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp 315 320 325	1372
ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu 330 335 340	1420
aag cag cat gaa gaa agc cta aga act att gag gct ctg aaa agt aga Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg 345 350 355	1468

**Figure 4-3**

ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg 1516  
Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg  
360 365 370 375

aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca 1564  
Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser  
380 385 390

cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg 1612  
Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met  
395 400 405

tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa 1660  
Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu  
410 415 420

aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat 1708  
Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp  
425 430 435

tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag 1756  
Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys  
440 445 450 455

gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag 1804  
Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu  
460 465 470

gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg 1852  
Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val  
475 480 485

cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca 1900  
Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr  
490 495 500

cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg 1948  
His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly  
505 510 515

aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa 1996  
Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys  
520 525 530 535

gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa 2044  
Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln  
540 545 550

atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc 2092  
Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly  
555 560 565

**Figure 4-4**

aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt	2140
Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys	
570 575 580	
gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc	2188
Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly	
585 590 595	
cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag	2236
Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu	
600 605 610 615	
aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag	2284
Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys	
620 625 630	
gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat	2332
Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn	
635 640 645	
gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg	2380
Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu	
650 655 660	
gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta	2428
Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu	
665 670 675	
gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg	2476
Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser	
680 685 690 695	
aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat	2524
Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn	
700 705 710	
aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat	2572
Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn	
715 720 725	
cat tac gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat	2620
His Tyr Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp	
730 735 740	
gta att gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa	2668
Val Ile Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys	
745 750 755	
tat aca gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc	2716
Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala	
760 765 770 775	

**Figure 4-5**

agt tta agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc Ser Leu Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro 780 785 790	2764
gag aga cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa Glu Arg His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu 795 800 805	2812
ctt aag aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa Leu Lys Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln 810 815 820	2860
gag aaa ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc Glu Lys Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr 825 830 835	2908
atg agt cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act Met Ser His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr 840 845 850 855	2956
gcc ttg agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg Ala Leu Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val 860 865 870	3004
aag aag aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat Lys Lys Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp 875 880 885	3052
gag aac gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta Glu Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val 890 895 900	3100
aaa gct gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc Lys Ala Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly 905 910 915	3148
cta agg aag agc atg aag gtc cag gac aac agc gct gaa ata ctg Leu Arg Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu 920 925 930 935	3196
gct aag tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag Ala Lys Tyr Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu 940 945 950	3244
att gca gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag Ile Ala Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys 955 960 965	3292
cta aaa tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt Leu Lys Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe 970 975 980	3340

**Figure 4-6**

aaa gcc act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag Lys Ala Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln 985 990 995	3388
aag tat aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat Lys Tyr Asn Thr Ser Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn 1000 1005 1010 1015	3436
gac aag tta aag aag gag atc ctc act ctt cag aag gat cta aag gat Asp Lys Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp 1020 1025 1030	3484
aag aat gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc Lys Asn Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser 1035 1040 1045	3532
aga aaa aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa Arg Lys Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys 1050 1055 1060	3580
tac aca gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc Tyr Thr Glu Ala Lys Lys Glu Lys Leu Val Glu Glu Asn Ala 1065 1070 1075	3628
aag cag act tct gag atc ctt gca gca caa act ctt ttg cag aag cag Lys Gln Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln 1080 1085 1090 1095	3676
cat gtt ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt His Val Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly 1100 1105 1110	3724
aca atc gag aca ctc aag gaa ctg aaa act aag cag aga tgt tat Thr Ile Glu Thr Leu Lys Glu Leu Lys Thr Lys Gln Arg Cys Tyr 1115 1120 1125	3772
gag aaa gag cag aca gtg acc caa ctg cgg cag atg ctg gag aat Glu Lys Glu Gln Gln Thr Val Thr Gln Leu Arg Gln Met Leu Glu Asn 1130 1135 1140	3820
cag aag aac tcc tct gtg ccc ctg gct gag cat ttg cag gtt aag gaa Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln Val Lys Glu 1145 1150 1155	3868
gca ttt gag aaa gaa gtt gga atc ata aaa gct agc ttg aga gaa aag Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu Arg Glu Lys 1160 1165 1170 1175	3916
gaa gaa gaa agc caa aac aaa act gaa gag gtc tcc aaa ctc cag tct Glu Glu Glu Ser Gln Asn Lys Thr Glu Glu Val Ser Lys Leu Gln Ser 1180 1185 1190	3964

**Figure 4-7**

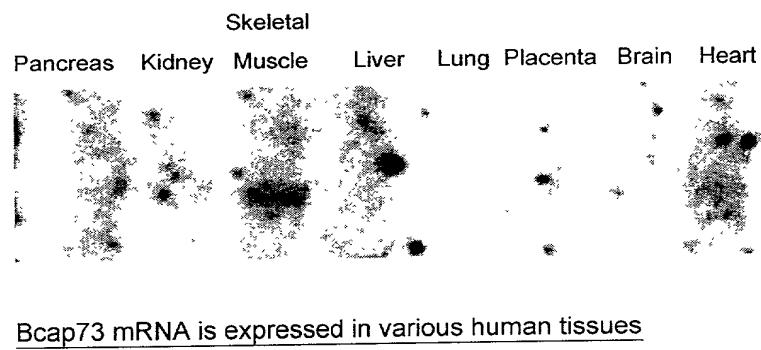
gag att cag aat act aaa caa gcg tta aaa aaa tta gag act cg <sup>g</sup> gag	4012		
Glu Ile Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu Thr Arg Glu			
1195	1200	1205	
gtg gtt gat ttg tcg aaa tat aaa gca acg aaa agc gat ttg gag aca	4060		
Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp Leu Glu Thr			
1210	1215	1220	
cag att tcc gac tta aac gaa aaa ttg gcc aat ctg aat agg aag tat	4108		
Gln Ile Ser Asp Leu Asn Glu Lys Leu Ala Asn Leu Asn Arg Lys Tyr			
1225	1230	1235	
gag gaa gta tgt gag gag gtt ttg cat gcc aaa aag aag gaa ctg tct	4156		
Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Glu Leu Ser			
1240	1245	1250	1255
gct aaa gat gag aag gaa ttg ctc cat ttc agc ata gag caa gaa atc	4204		
Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu Gln Glu Ile			
1260	1265	1270	
aaa gat cag cag gaa cga tgt gac aaa tcc tta aca acc atc acg gag	4252		
Lys Asp Gln Gln Glu Arg Cys Asp Lys Ser Leu Thr Thr Ile Thr Glu			
1275	1280	1285	
cta cag aga aga ata cag gaa tct gcc aaa caa atc gaa gca aaa gat	4300		
Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu Ala Lys Asp			
1290	1295	1300	
aat aag ata act gaa ctg ctc aat gat gtg gag aga tta aaa cag gcc	4348		
Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu Lys Gln Ala			
1305	1310	1315	
ctc aat ggc ctt tcc cag ctc acc tat gga agt ggg agt ccc agc aag	4396		
Leu Asn Gly Leu Ser Gln Leu Thr Tyr Gly Ser Gly Ser Pro Ser Lys			
1320	1325	1330	1335
agg cag agt cag ctg att gac agc ctg cag cag cag gtc agg tcc ctg	4444		
Arg Gln Ser Gln Leu Ile Asp Ser Leu Gln Gln Val Arg Ser Leu			
1340	1345	1350	
cag cag cag ctg gcg gat gcc gac aga cag cac caa gaa gta att gca	4492		
Gln Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu Val Ile Ala			
1355	1360	1365	
att tat cgg aca cac ctt ctt agt gct gca cag ggt cac atg gat gag	4540		
Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His Met Asp Glu			
1370	1375	1380	
gat gtg cag gcc gcc tta ctg cag atc ata cag atg cg <sup>g</sup> cag ggg ctc	4588		
Asp Val Gln Ala Ala Leu Leu Gln Ile Ile Gln Met Arg Gln Gly Leu			
1385	1390	1395	

### Figure 4-8

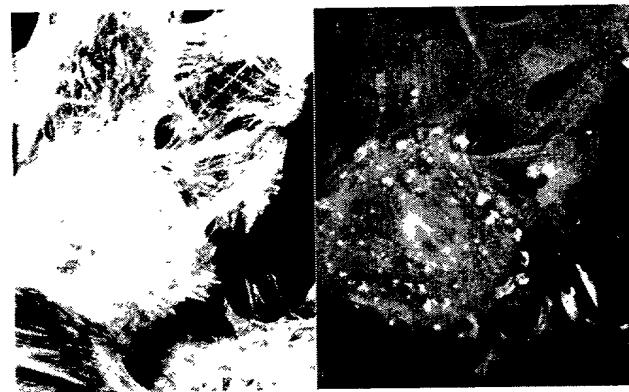
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Val Cys  
1400

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gtatTTTgat ccatcaaaaa aaaaaaaaaa aa 4736

**Figure 5**

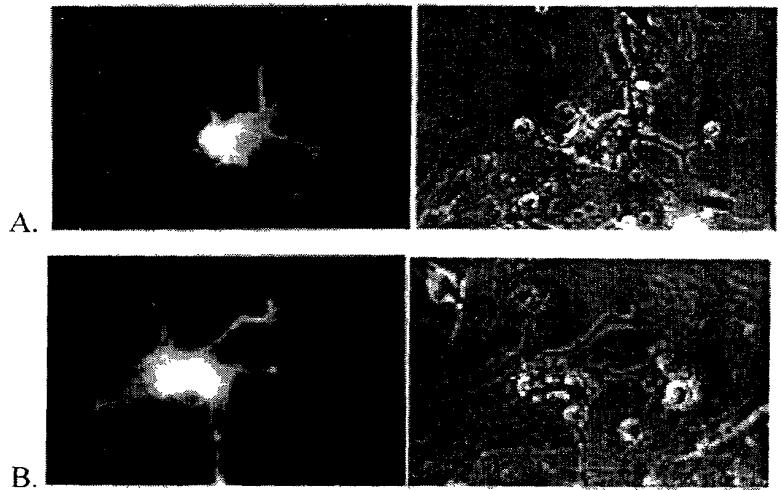


**Figure 6**



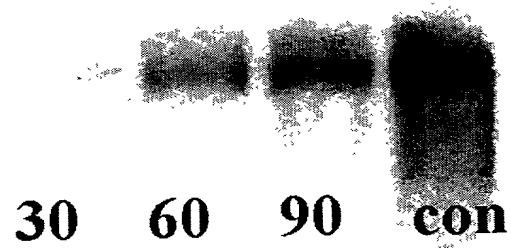
Overexpression of recombinant bcap73 induces formation of novel membrane protrusions

**Figure 7**



Overexpression of bcap73 domains induces aberrant cellular projections

**Figure 8**



Bcap73 mRNA is down-regulated in response to injury

### Figure 9-1

Sequence Alignment of *bcap73* cDNA against Canine familiaris mRNA for C3VS protein (GenBank accession X99145)

Query=βCAP73

Sbjct=C3VS

Query: 358 tttgctgttagcaacaagaaaactaaatcctgtctatgatgagctgtggtttcttgtc 417  
Sbjct: 12 tttgctgctagcaaccagaaaaccatcctgtctatgatgaactgtggtttcttgtc 71

Query: 418 tcctaagaacagacaaggcagcagattgaaacaatacgatgaccgattgatgagagcgc 477  
Sbjct: 72 tcccaagaacagacatgcagcagattgaaacaatacgatgaccgattgatgaaagccgc 131

Query: 478 agaaaggggagatgtagaaaaagtgtcctcaatcctgctaaaaagggagtcaatccagg 537  
Sbjct: 132 ggagaggggagatgtagaaaaagttcctcaatcctgctaaaaagggcatcaatccagg 191

Query: 538 caagcttagatgtagaaggcagatctgccttcatgttgtggctcaaaggaaatcttga 597  
Sbjct: 192 caaacttagatgtggaaaggcagatctgccttcatgttgtggctcaaaggaaatcttga 251

Query: 598 gtgttgaatgccatcctcatacatggagttgatattacaaccagtgacaccgcaggaag 657  
Sbjct: 252 atgtttgaatgccatcctcatacatggagttgatattacaaccagtgacactgcaggaag 311

Query: 658 gaatgctttcacctggctgcaaagtatgggcatgcactgtgtctacaaaaacttctaca 717  
Sbjct: 312 aaatgctttcacttggctgcaaagtatgggcatgcattgtgtctacaaaaacttctaca 371

Query: 718 gtacaattgtcccactgaacatgttagacactgcagggaaagaactgcacttcatgtgcgc 777  
Sbjct: 372 gtacaattgtcccactgaacatgcagacactgcagggaaagaaccgcacttcatgcgc 431

Query: 778 tatggcagactgtcctttagcatacagactgtgtctgcgaccatgggcctcggtgaatgc 837  
Sbjct: 432 aatggcagactgtccttcagcatacagactgtgtgtgaccatgggcctccgtgaatgc 491

Query: 838 caaagatgttagatggcgacaccacttggctggctacccagatgttaggcacaaat 897  
Sbjct: 492 caaagatgtggatggcgacaccgcgtggctggctactcagatgttaggcacaaat 551

**Figure 9-2**

Query: 898 atgtcaactgctgatagatagaggggcggatattaattccagagacaaacaaaacaggac 957  
Sbjct: 552 ctgtcaactgctgatagatcgagggcagagattaattccagagacaaacaaaacagaac 611

Query: 958 tgctctcatgcttaggatgcgagtatggttgcaaagatgcagtagaagtcttaatcaaaaa 1017  
Sbjct: 612 tgctctcatgctgggtgcagtatggttgaaggatgctgtagaagtcttacttaaaaa 671

Query: 1018 cggcgctgacgtgaccttgctggacgccttggccatgacagttcttactatgcaagaat 1077  
Sbjct: 672 tggtgctgatgtaaagcctgctggatgcctggccatgatagttcttactatgcaagaat 731

Query: 1078 tgggacaatctggacattctaaccattactgaagactgcatcagaaaattccaacaaagg 1137  
Sbjct: 732 tgggacaatctggacattctaactttattgaagactgcgtcagaaaatccaacaaagg 791

Query: 1138 gagagaactttggaagaaaggaccatcttacaacagcgaaattgtctcagatgctaga 1197  
Sbjct: 792 gagagaactttggaagaaaggaccatcttacagcagcgaaatttgcgtacatgctaga 851

Query: 1198 tgaagtaatacgaagtcaaattcagaggagcatcaaaacattcaggatctggagattga 1257  
Sbjct: 852 tgaagtaatgtgaagtcaagtcaaggcagggagcatcgaaacattcaggagctggagattga 911

Query: 1258 aaatgaagatctgaaagagagattgagaaaaattcagcaagaacagagaatattttgga 1317  
Sbjct: 912 aaatgaagatttggaaagacaggttggaaaaattcagcaagaacagagaatattactgga 971

Query: 1318 taaagtcaatggttacagctacagctgaatgaggaagtaatggggctgatgtctgga 1377  
Sbjct: 972 taaagtcaatggttacaactacagctgaatgaggaagttgatggggctgatgtctgga 1031

Query: 1378 aagtgagaaaagaaaagctgaagtccctttggcagccaaagaaaagcagcatgaagaaaag 1437  
Sbjct: 1032 aagtgagaaaagaaaagctgaagtctctttggctaaagaaaagcaacatgaagaaaag 1091

Query: 1438 cctaagaactattgaggctctgaaaagttagatttaagtattttgag 1483  
Sbjct: 1092 cctaagaactattgaggctctgaaaacagatttaaatattttgag 1137

**Figure 9-3**

Query: 1566 agtgtacttccacaggcatgcacgtccatatgcaaagccatctatgttaagaccactgg 1625  
Sbjct: 1136 agtgtacttccccaggggtgcacagccacatgcaaaggcaggtctatgttaagaccactgg 1195

Query: 1626 agcttagccttacctaattcaaggctcatattcgaaaacgaaattttaagaaaatttag 1685  
Sbjct: 1196 agctatcattacccaatcaaaccctcatattgtaaaatgacctcttaagaaaagatgttag 1255

Query: 1686 aagcaatgagaactttctgtgattcagcaaaacaagacagactcaaactccaaaatgaac 1745  
Sbjct: 1256 aagcaatgagaactttctgcgaatcagccaaacaagaccgcctcaagctccagaacggag 1315

Query: 1746 tggctcacaagggtggcgagggtgcaaggccttagcattggaatgtgaaagggtgaaaggagg 1805  
Sbjct: 1316 tggcgcacaagggtggctgagtgcaaagctttaggactagaatgtgaacgcataaggagg 1375

Query: 1806 attcagatgagcagataaagcaactagaagatgccttggaaagacgtgcagaagagaatgt 1865  
Sbjct: 1376 actctgatgagcagataaagcagttttagaagacgcattggaaagatgtgcagaagagaatgt 1435

Query: 1866 atgagtccggaaaggtaaaatgtgaaacaaaatgcagacacatttctgccttggaaaggaggcacc 1925  
Sbjct: 1436 atgagtccggaaaggtaaaacaaaatgcagacacacttctgccttggaaaggaggcacc 1495

Query: 1926 tgacaagtgtatgcggccactggaaaccacaggctgtggaggaactgaaggatcagtta 1985  
Sbjct: 1496 tgaccagtgtatggaaatcacagactatggaggagctgtggaaaggatcagtta 1555

Query: 1986 aagacatgaaagtgaaatacgaagggtgcgtccgcagaagtggggaaattgagaaaccaa 2045  
Sbjct: 1556 aggacatgaaagcgaataatgagggtgcatacagactatggaggagctgtggaaaggaggaa 1615

Query: 2046 tcaaacaaaatgaaatgttagttgtggaaaggatgtggaggatgaggcaagctgtggaa 2105  
Sbjct: 1616 tcaaacaaaatgagctgttagtgcatacagatgtggaggatgtggcaagctgtggaa 1675

Query: 2106 agaataagcgactgcagaaggagggtggacatgtgtggaggcgagagaagagaggaa 2165  
Sbjct: 1676 agaataagcgattgcagaaggactcagttgtggaaacggaggcgagacaagaaaggaa 1735

### Figure 9-4

Query: 2166 ggaagctoactgagatggaaggccagttaaaggacttgtcagccaagctggcccttcta 2225  
Sbjct: 1736 ggagggttgctgaggtggaaggccaggtaaaggaactcttagcaaagctgaccttgcag 1795

Query: 2226 ttccagcagagaaaattgaaaacatgaagagcttgttatcaa 2267  
Sbjct: 1796 ttccaactgaaaaattttagagcatgaagagcttattatcaa 1837

## Figure 10-1

Sequence Alignment of bcap73 against Tentative Human Concensus (THC) Contiguous Sequences  
THC244788 THC143090 THC186491 THC213238 (from TIGR)

Score = 1052 bits (547), Expect = 0.0

Identities = 905/1092 (82%), Positives = 905/1092 (82%), Gaps = 4/1092 (0%)

Query=bcap73 cDNA

Sbjct=THC seq

Query: 3136 aaagatgagtggcctaaggaagagcatgaagaaggccaggacaacagcgctgaaatact 3195  
Sbjct: 6 aaagatgagctcgctaagtcagagcatgagaaaggtscaggatagtaatgctgaaatctt 65

Query: 3196 ggctaagtacnnnnnnngccaggaggattgtcacccctgcatgaggagattgcagccca 3255  
Sbjct: 66 ggccamctacagaaaaggccaagaagagattgtgacactkcatgccaaattaragccca 125

Query: 3256 gaagagagaactcgacacgatacaggaatgcatcaagctaaaatatgctccgatcatcag 3315  
Sbjct: 126 gargarlagctcgacacaatacagartgcattaaggtaaaaatgccccattgtcag 185

Query: 3316 cttggaagagtgtgagagaaaattaaagccactgagaaagaac-taaaagaacagctat 3374  
Sbjct: 186 ctttgaggagtscgagagaaaattaaagcaacagagaaagaacctaaaagaccagttat 245

Query: 3375 cccagcagacacagaagtataataccagtgaagaagaggccaagaagtgc当地 3434  
Sbjct: 246 cagagcagacacaaaagtatagtgtcagtgaagaagtcaagaaaaacaagcaagaga 305

Query: 3435 atgacaagttaaagaaggagatcctcactttcagaaggatctaaaggataagaatgttc 3494  
Sbjct: 306 atgacaagttaaagaaggagattttacccttcagaaagatgtgagagayaagacagttc 365

Query: 3495 acattgagaattcttatgaaacagaaagagcattaagcagaaaaacagaagagctgaaca 3554  
Sbjct: 366 tcattgagaagtctcatgaaatggaaagagcattaagcagaaaaacagacagctaaaca 425

Query: 3555 gacagttaaaagacctgtcgagaaatacacagaggaaagaaggagaaagagaagctcg 3614  
Sbjct: 426 aacagttaaaagacttgtcacagaaatacacggaagtaagaatgtgaaagagaagctag 485

**Figure 10-2**

Query: 3615 tggaggaaaatgccaagcagacttctgagatcctgcagcacaaactctttcagaac 3674  
Sbjct: 486 tagaagaaaatgccaaacagacttctgagatacttgcagtgcaaaatctttcaaaaac 545

Query: 3675 agcatgttccgctggagcaggtttagtccctgaaaaatctcttagtggtacaatcgaga 3734  
Sbjct: 546 aacatgttccattggaacaggtttaggctctgaaaaatctcttaatggcacaattgaaa 605

Query: 3735 cactcaaggaagaactgaaaactaaggcagagatgttatgagaaagagcagcagacagtga 3794  
Sbjct: 606 atctaaaggaagaactgaagagtatgcaaagggttacgagaaagagcagcagacagtga 665

Query: 3795 cccaaactgcggcagatgctggagaatcagaagaactcctctgtgccccctggctgaggcatt 3854  
Sbjct: 666 cccaaactgcatcaattgttggagaatcaaaagaactttctgtacccctggcagagcatt 725

Query: 3855 tgcaggtaaggaagcattttagaaagaagttttagatcataaaagcttagttgagagaaa 3914  
Sbjct: 726 tgcagattaaagaagcattttagaaagaagttttagatcataaaagccagttgagagaaa 785

Query: 3915 aggaagaagaaagccaaaacaaaactgaagaggctccaaactccaggctgagattcaga 3974  
Sbjct: 786 aggaagaagaaagccaaaacaaaatgaaagaagttttagatcataaaagccagttgagagaaa 845

Query: 3975 atactaaacaagcgtnnnnnnnnttagagactcgggagggtggattgtcgaaatata 4034  
Sbjct: 846 atactaaacaagcmtaaaaaaatttagagactagagaggtagttactgtctaaatata 905

Query: 4035 aagcaacgaaaagcgatttggagacacagattccgacttaacgaaaaattggccaatc 4094  
Sbjct: 906 aagcaacaaaaagtgatttggagacacagattcttagcttaatgaaaaattggccaatc 965

Query: 4095 tgaataggaagtatgaggaagtatgttagggaggtttgcattgcacaaaagaaggaactgt 4154  
Sbjct: 966 tgaatagaaaagtatgaggaagt-tgttagggaggtttgcattgcacaaaagaaggaatata 1024

Query: 4155 ctgctaaagatgagaaggaattgtccatttcagcatagagcaagaaatcaaagatcagc 4214  
Sbjct: 1025 ctgscaaagatgagaagga-ttactgc-tttcaccttgagscaggaaatataagggtcagr 1082

**Figure 10-3**

Query: 4215 aggaacgatgtg 4226  
          |||||||||||||  
Sbjct: 1083 aggaacgatgtg 1094